IFWO

RAW SEQUENCE LISTING   DATE: 08/30/2004
PATENT APPLICATION: US/10/759,463   TIME: 14:42:30

Input Set : **N:\Crf3\RULE60\10759463.raw.txt**
Output Set: **N:\CRF4\08302004\J759463.raw**

```
 1 <110> APPLICANT: Itadani, Hiraku
 2        Takimura, Tetsuo
 3        Nakamura, Takao
 4        Kobayashi, Masahiko
 5        Tanaka, Ken-ichi
 6        Hidaka, Yusuke
 7        Ohta, Masataka
 8 <120> TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
 9        BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
10 <130> FILE REFERENCE: 06501-083001
11 <140> CURRENT APPLICATION NUMBER: US/10/759,463
12 <141> CURRENT FILING DATE: 2004-01-16
13 <150> PRIOR APPLICATION NUMBER: US/09/891,053
14 <151> PRIOR FILING DATE: 2001-06-25
15 <150> PRIOR APPLICATION NUMBER: PCT/JP99/07280
16 <151> PRIOR FILING DATE: 1999-12-24
17 <150> PRIOR APPLICATION NUMBER: PCT/JP98/05967
18 <151> PRIOR FILING DATE: 1998-12-25
19 <150> PRIOR APPLICATION NUMBER: JP 11/145661
20 <151> PRIOR FILING DATE: 1999-05-25
21 <160> NUMBER OF SEQ ID NOS: 26
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 413
26 <212> TYPE: PRT
27 <213> ORGANISM: Rattus norvegicus
28 <400> SEQUENCE: 1
29        Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu
30         1               5                  10                  15
31        Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
32                        20                  25                  30
33        Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
34                    35                  40                  45
35        Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser
36             50                  55                  60
37        Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp
38        65                  70                  75                  80
39        Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu
40                        85                  90                  95
41        Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val
42                        100                 105                 110
43        Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile
44                    115                 120                 125
```

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```
45        Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala
46            130                 135                 140
47        Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp
48        145                 150                 155                 160
49        Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr
50                        165                 170                 175
51        Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe
52                    180                 185                 190
53        Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe
54                195                 200                 205
55        Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn
56            210                 215                 220
57        Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly
58        225                 230                 235                 240
59        Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro
60                        245                 250                 255
61        Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu
62                    260                 265                 270
63        His Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu
64                    275                 280                 285
65        Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg
66                290                 295                 300
67        Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg
68        305                 310                 315                 320
69        Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly
70                        325                 330                 335
71        Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys
72                    340                 345                 350
73        His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu
74                355                 360                 365
75        Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His
76            370                 375                 380
77        Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu
78        385                 390                 395                 400
79        Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys
80                        405                 410
82 <210> SEQ ID NO: 2
83 <211> LENGTH: 1239
84 <212> TYPE: DNA
85 <213> ORGANISM: Rattus norvegicus
86 <220> FEATURE:
87 <221> NAME/KEY: CDS
88 <222> LOCATION: (1)...(1239)
89 <400> SEQUENCE: 2
90        atg gag cgc gcg ccg ccc gac ggg ctg atg aac gcg tcg ggc act ctg        48
91        Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu
92        1                   5                   10                  15
93        gcc gga gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc        96
94        Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
```

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Input Set : **N:\Crf3\RULE60\10759463.raw.txt**
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```
 95                 20                25               30
 96    tgg acc gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca    144
 97    Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
 98             35                40                45
 99    gta ctg ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tcg agc    192
100    Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser
101         50                  55                60
102    ctc cgc acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac    240
103    Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp
104    65                  70                75                80
105    ttc ctc gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg    288
106    Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu
107                 85                90                95
108    acc ggc cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg    336
109    Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val
110                 100               105               110
111    gta gac tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gta ctc atc    384
112    Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile
113             115                120               125
114    agc tat gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc    432
115    Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala
116         130                 135               140
117    cag cag ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg    480
118    Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp
119    145                 150               155               160
120    gtg ctg gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac    528
121    Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr
122                 165               170               175
123    ctg tct ggt ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc    576
124    Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe
125                 180               185               190
126    ttc tac aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc    624
127    Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe
128             195                200               205
129    acg ccc ttc ctc agc gtt acc ttc ttc aac ctc agc atc tac ctg aac    672
130    Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn
131         210                 215               220
132    atc cag agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc    720
133    Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly
134    225                 230               235               240
135    cca gaa ccc cca cca gat gcc cag ccc tcg cca cct cca gct ccc ccc    768
136    Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro
137                 245               250               255
138    agc tgc tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg    816
139    Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu
140                 260               265               270
141    cac agc tct ggc agc tcc tca agg ggc act gag agg cca cgc tca ctc    864
142    His Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu
143             275                280               285
```

```
144         aaa agg ggc tcc aag cca tca gca tct tca gca tcc ctg gag aag cgc        912
145         Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg
146             290                 295                 300
147         atg aag atg gtg tcc cag agc atc acc cag cgc ttc cgg ctg tcg cgg        960
148         Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg
149         305                 310                 315                 320
150         gac aag aag gtg gcc aag tcg ctg gcc atc atc gtg agc atc ttt ggg        1008
151         Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly
152             325                 330                 335
153         ctc tgc tgg gcg ccg tac acg ctc cta atg atc atc cga gct gct tgc        1056
154         Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys
155             340                 345                 350
156         cat ggc cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg ctt        1104
157         His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu
158             355                 360                 365
159         ctg tgg gcc aac tcg gcc gtc aac ccc gtc ctc tac cca ctg tgc cac        1152
160         Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His
161             370                 375                 380
162         tac agc ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc        1200
163         Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu
164         385                 390                 395                 400
165         aag gtc cag ccc cac ggc tcc ctg gag cag tgc tgg aag                    1239
166         Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys
167             405                 410
```

```
169 <210> SEQ ID NO: 3
170 <211> LENGTH: 21
171 <212> TYPE: DNA
172 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: artificially synthesized primer sequence
W--> 175 <221> NAME/KEY: misc_feature
176 <222> LOCATION: (1)...(21)
177 <223> OTHER INFORMATION: n = A,T,C or G
W--> 178 <400> 3
W--> 179      batngccaac ctbkccttct c                                            21
181 <210> SEQ ID NO: 4
182 <211> LENGTH: 20
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: artificially synthesized primer sequence
W--> 187 <221> NAME/KEY: misc_feature
188 <222> LOCATION: (1)...(20)
189 <223> OTHER INFORMATION: n = A,T,C or G
W--> 190 <400> 4
W--> 191      ccataaaagn ngggggttgac                                             20
193 <210> SEQ ID NO: 5
194 <211> LENGTH: 2700
195 <212> TYPE: DNA
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            Input Set : N:\Crf3\RULE60\10759463.raw.txt
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196 <213> ORGANISM: Rattus norvegicus
197 <220> FEATURE:
198 <221> NAME/KEY: CDS
199 <222> LOCATION: (351)...(1589)
200 <221> NAME/KEY: misc_feature
201 <222> LOCATION: (1)...(2700)
202 <223> OTHER INFORMATION: n = A,T,C or G
203 <400> 5
204   aattcggcac gagcgggcag atcgcggggc gcactcggtt gcgcgctgag ctaggggtgc   60
205   accgacgcac cgcgggcggc tggagctcgg ctttgctctc gctgcagcag ccgcgccgcc   120
206   cgccccactc cgctcagatt ccgacaccag ccccctctgg atcgccctcc tggactctag   180
207   cccgggctct tgctccgacc ccgcggacca tgctccgggc gccccccgga aaaccgggct   240
208   gggcgaagag ccggcaaaga ttaggctcac gagcggggc cccacccggc cacccagctc   300
209   tccgcccgtg ccctgcccgg tgtccccgag ccgtgtgagc ctgctgggcc atg gag   356
210   Met Glu
211   1
212   cgc gcg ccg ccc gac ggg ctg atg aac gcg tcg ggc act ctg gcc gga   404
213   Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu Ala Gly
214   5   10   15
215   gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc tgg acc   452
216   Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala Trp Thr
217   20   25   30
218   gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca gta ctg   500
219   Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr Val Leu
220   35   40   45   50
221   ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tcg agc ctc cgc   548
222   Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser Leu Arg
223   55   60   65
224   acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac ttc ctc   596
225   Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp Phe Leu
226   70   75   80
227   gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg acc ggc   644
228   Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu Thr Gly
229   85   90   95
230   cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg gta gac   692
231   Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val Val Asp
232   100   105   110
233   tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gta ctc atc agc tat   740
234   Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile Ser Tyr
235   115   120   125   130
236   gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc cag cag   788
237   Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala Gln Gln
238   135   140   145
239   ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg gtg ctg   836
240   Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp Val Leu
241   150   155   160
242   gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac ctg tct   884
243   Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr Leu Ser
244   165   170   175

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/30/2004
PATENT APPLICATION: **US/10/759,463**   TIME: 14:42:31

Input Set : **N:\Crf3\RULE60\10759463.raw.txt**
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<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 4
Seq#:4; N Pos. 10,11
Seq#:5; N Pos. 2688
Seq#:11; N Pos. 20
Seq#:22; N Pos. 18
Seq#:23; N Pos. 18

VERIFICATION SUMMARY   DATE: 08/30/2004
PATENT APPLICATION: **US/10/759,463**   TIME: 14:42:31

Input Set : **N:\Crf3\RULE60\10759463.raw.txt**
Output Set: **N:\CRF4\08302004\J759463.raw**

```
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:175 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:178 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:187 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:190 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:203 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:2629
L:365 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
L:366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:679 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:682 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
L:683 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:691 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:694 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
L:695 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0
```